

Amendments to the Claims:

1. (Currently amended) A method of reducing pathogenicity to a plant of a fungus that produces fumonisin, comprising:
 - a) stably integrating into the genome of a plant cell a first nucleotide sequence operably linked to a promoter active in said plant cell, wherein said first nucleotide sequence has at least 95% sequence identity to the sequence set forth in SEQ ID NO: 16, 18, 20, 22, 24, 26, 28, 30, or 32 and encodes a polypeptide having amine oxidase activity;
 - b) optionally stably integrating into the genome of said plant cell a second nucleotide sequence operably linked to a promoter active in said plant cell, wherein said second nucleotide sequence has at least 95% sequence identity to the sequence set forth in SEQ ID NO: 12 or 14 and encodes a polypeptide having fumonisin esterase activity; and
 - c) stably integrating into the genome of said plant cell a nucleotide sequence operably linked to a promoter active in said plant cell, wherein said nucleotide sequence has at least 95% sequence identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10, and encodes a polypeptide having fumonisin detoxification activity; and
 - d) regenerating a transformed plant from said plant cell,
whereby the pathogenicity of said fungus to said transformed plant is reduced in comparison to
the pathogenicity of said fungus to a plant that has not been transformed.
2. (Previously presented) The method of claim 1, wherein said second nucleotide sequence comprises the sequence set forth in SEQ ID NO: 12 or 14.
3. (Previously presented) The method of claim 1, wherein the nucleotide sequence of step (c) comprises the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.
4. (Previously presented) The method of claim 1, wherein said first nucleotide sequence comprises the sequence set forth in SEQ ID NO: 16, 18, 20, 22, 24, 26, 28, 30, or 32.

5. (Previously presented) The method of claim 1, wherein said plant cell is a cell from a monocot.

6. (Original) The method of claim 5, wherein said monocot is maize.

7. (Previously presented) The method of claim 1, wherein said plant cell is a cell from a dicot.

8. (Previously presented) The method of claim 1, wherein the promoter of step (a) is an inducible promoter.

9. (Previously presented) The method of claim 8 further comprising inducing expression of said first nucleotide sequence for a time sufficient to reduce pathogenicity of said fungus.

10. (Previously presented) A plant having stably integrated into its genome:

a) a first nucleotide sequence operably linked to a promoter active in said plant, wherein said first nucleotide sequence has at least 95% sequence identity to the sequence set forth in SEQ ID NO: 16, 18, 20, 22, 24, 26, 28, 30, or 32 and encodes a polypeptide having amine oxidase activity;

b) optionally, a second nucleotide sequence operably linked to a promoter active in said plant, wherein said second nucleotide sequence has at least 95% sequence identity to the sequence set forth in SEQ ID NO: 12 or 14 and encodes a polypeptide having fumonisin esterase activity; and,

c) a nucleotide sequence operably linked to a promoter active in said plant, wherein said nucleotide sequence has at least 95% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10, and encodes a polypeptide having fumonisin detoxification activity.

11. (Previously presented) The plant of claim 10, wherein said second nucleotide sequence is set forth in SEQ ID NO: 12 or 14.

12. (Previously presented) The plant of claim 10, wherein said first nucleotide sequence encodes a polypeptide having the sequence set forth in SEQ ID NO: 17, 19, 21, 23, 25, 27, 29, 31, or 33.

13. (Previously presented) The plant of claim 10, wherein said first nucleotide sequence comprises the sequence set forth in SEQ ID NO: 16, 18, 20, 22, 24, 26, 28, 30, or 32.

14. (Original) The plant of claim 10, wherein said plant is a monocot.

15. (Original) The plant of claim 14, wherein said monocot is maize.

16. (Original) The plant of claim 10, wherein said plant is a dicot.

17. (Previously presented) Transformed seed of the plant of claim 10.

18. (Previously presented) A plant cell having stably integrated into its genome:
a) a first nucleotide sequence operably linked to a promoter active in said plant cell, wherein said first nucleotide sequence has at least 95% sequence identity to the sequence set forth in SEQ ID NO: 16, 18, 20, 22, 24, 26, 28, 30, or 32 and encodes a polypeptide having amine oxidase activity;

b) optionally, a second nucleotide sequence operably linked to a promoter active in said plant cell, wherein said second nucleotide sequence has at least 95% sequence identity to the sequence set forth in SEQ ID NO: 12 or 14 and encodes a polypeptide having fumonisin esterase activity; and,

c) a nucleotide sequence operably linked to a promoter active in said plant cell, wherein said nucleotide sequence has at least 95% identity to the sequence set forth in

SEQ ID NO: 2, 4, 7, or 10 and encodes a polypeptide having fumonisin detoxification activity.

19. (Currently amended) A method of reducing pathogenicity to a plant of a fungus that produces fumonisin, comprising stably integrating into the genome of a plant cell:

- a) a first nucleotide sequence operably linked to a promoter active in said plant cell, wherein said first nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 17, 19, 21, 23, 25, 27, 29, 31, or 33 and having amine oxidase activity;
- b) optionally, a second nucleotide sequence operably linked to a promoter active in said plant cell, wherein said second nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 13 or 15 and having fumonisin esterase activity; and,
- c) a nucleotide sequence operably linked to a promoter active in said plant cell, wherein said nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 3, 5, 8, or ~~10~~ 11, and having fumonisin detoxification activity; and
- d) regenerating a transformed plant from said plant cell,

whereby the pathogenicity of said fungus to said transformed plant is reduced in comparison to the pathogenicity of said fungus to a plant that has not been transformed.

20. (Currently amended) A plant having stably integrated into its genome

- a) a first nucleotide sequence operably linked to a promoter active in said a plant cell, wherein said first nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 17, 19, 21, 23, 25, 27, 29, 31, or 33 and having amine oxidase activity;
- b) optionally, a second nucleotide sequence operably linked to a promoter active in said a plant cell, wherein said second nucleotide sequence encodes a polypeptide

having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 13 or 15 and having fumonisin esterase activity; and,

c) a nucleotide sequence operably linked to a promoter active in ~~said~~ a plant cell, wherein said nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 3, 5, 8, or 11 and having fumonisin detoxification activity.

21. (Previously presented) The method of claim 1, wherein the nucleotide sequence of step (c) has at least 98% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

22. (Previously presented) The method of claim 1, wherein the nucleotide sequence of step (c) encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.

23. (Previously presented) The plant cell of claim 18, wherein said first nucleotide sequence is set forth in SEQ ID NO: 16, 18, 20, 22, 24, 26, 28, 30, or 32.

24. (Previously presented) The plant of claim 10, wherein the nucleotide sequence of step (c) encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.

25. (Previously presented) The plant of claim 10, wherein the nucleotide sequence of step (c) is the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

26. (Previously presented) The plant cell of claim 18, wherein said first nucleotide sequence has at least 98% sequence identity to the sequence set forth in SEQ ID NO: 16, 18, 20, 22, 24, 26, 28, 30, or 32, said second nucleotide sequence has at least 98% sequence identity to the sequence set forth in SEQ ID NO: 12 or 14, and the nucleotide sequence of step (c) has at least 98% identity to the sequence set forth in SEQ ID NO: 2, 4, 7, or 10.

27. (Previously presented) The plant cell of claim 18, wherein the nucleotide sequence of step (c) encodes the polypeptide set forth in SEQ ID NO: 3, 5, 8, or 11.

28. (Previously presented) The plant cell of claim 18, wherein said first nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 17, 19, 21, 23, 25, 27, 29, 31, or 33, said second nucleotide sequence encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 13 or 15, and the nucleotide sequence of step (c) encodes a polypeptide having at least 95% sequence identity to the sequence set forth in SEQ ID NO: 3, 5, 8, or 11.

29. (Previously presented) The method of claim 1, wherein said first nucleotide sequence encodes a polypeptide having the sequence set forth in SEQ ID NO: 13 or 15, said second nucleotide sequence encodes a polypeptide having the sequence set forth in SEQ ID NO: 17, 19, 21, 23, 25, 27, 29, 31, or 33, and the nucleotide sequence of step (c) encodes a polypeptide having the sequence set forth in SEQ ID NO: 3, 5, 8, or 11.

30. (Previously presented) The plant cell of claim 18, wherein said first nucleotide sequence encodes a polypeptide comprising the sequence set forth in SEQ ID NO: 17, 19, 21, 23, 25, 27, 29, 31, or 33, said second nucleotide sequence encodes a polypeptide comprising the sequence set forth in SEQ ID NO: 13 or 15, and the nucleotide sequence of step (c) encodes a polypeptide comprising the sequence set forth in SEQ ID NO: 3, 5, 8, or 11.

31. (Previously presented) The plant cell of claim 18, wherein the nucleotide sequence of step (c) is set forth in SEQ ID NO: 2, 4, 7, or 10.

32. (Previously presented) The plant of claim 10, wherein said first nucleotide sequence encodes a polypeptide comprising the sequence set forth in SEQ ID NO: 17, 19, 21, 23, 25, 27, 29, 31, or 33, said second nucleotide sequence encodes a polypeptide comprising the sequence

set forth in SEQ ID NO: 13 or 15, and the nucleotide sequence of step (c) encodes a polypeptide comprising the sequence set forth in SEQ ID NO: 3, 5, 8, or 11.

33. (Previously presented) The plant cell of claim 18, wherein said second nucleotide sequence is set forth in SEQ ID NO: 12 or 14.